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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: THE SCRIPPS RESEARCH INSTITUTE
- (B) STREET: 10550 North Torrey Pines Road
- (C) CITY: La Jolla
- (D) STATE: California
- (E) COUNTRY: US
- (F) ZIP: 92037
- (G) TELEPHONE: (619) 784-2937
- (H) TELEFAX: (619) 784-9399

(ii) TITLE OF INVENTION: MHC CLASS II ANTIGEN PRESENTING SYSTEMS
AND METHODS FOR ACTIVATING CD4+ T CELLS

(iii) NUMBER OF SEQUENCES: 56

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US97/
- (B) FILING DATE: 22-MAY-1997
- (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/018,175
- (B) FILING DATE: 23-MAY-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTCGATGCA CACTCACATT CTTCTCCTAA TACGATAATA AAAC TTTCCA TGAAAAATAT	60
GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC TTAATTAAAA	120
TAGATAAATG GGAGCGGCTG GAATGGCGGA GCATGACCAA GTTCCTCCGC CAATCAGTCG	180
TAAACAGAA GTCGTGGAAG GCGGATAGAA AGAATGTTCCG ATTTGACGGG CAAGCATGTC	240
TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT CATGACCAAG	300
AATATAGCGG TGTGAGTGAG CGGGAAGCTC GGTTTCTGTC CAGATCGAAC TCAAACTAG	360
TCCAGCCAGT CGCTGTCGAA ACTAATTAAG TTAATGAGTT TTTCATGTTA GTTTCGCGCT	420
GAGCAACAAT TAAGTTTATG TTTCAGTTCC GCTTAGATTT CGCTGAAGGA CTTGCCACTT	480
TCAATCAATA CTTAGAACA AAATCAAAAC TCATTCTAAT AGCTTGGTGT TCATCTTTTT	540
TTTTAATGAT AAGCATTTTG TCGTTTATAC TTTTATATT TCGATATTAA ACCACCTATG	600
AAGTTCATTT TAATCGCCAG ATAAGCAATA TATTGTGTAA ATATTTGTAT TCTTTATCAG	660
GAAATTCAGG GAGACGGGGA AGTTACTATC TACTAAAAGC CAAACAATTT CTTACAGTTT	720
TACTCTCTCT ACTCTAGAGT	740

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGTTGC AGGACAGGAT GTGGTGCCCG ATGTGACTAG CTCTTTGCTG CAGGCCGTCC	60
TATCCTCTGG TTCCGATAAG AGACCCAGAA CTCCGGCCCC CCACCGCCCA CCGCCACCCC	120

CATACATATG TGGTACGCAA GTAAGAGTGC CTGCGCATGC CCCATGTGCC CCACCAAGAG	180
TTTTGCATCC CATACAAGTC CCCAAAGTGG AGAACCGAAC CAATTCTTCG CGGGCAGAAC	240
AAAAGCTTCT GCACACGTCT CCACTCGAAT TTGGAGCCGG CCGGCGTGTG CAAAAGAGGT	300
GAATCGAACG AAAGACCCGT GTGTAAAGCC GCGTTTCCAA AATGTATAAA ACCGAGAGCA	360
TCTGGCCAAT GTGCATCAGT TGTGGTCAGC AGCAAAATCA AGTGAATCAT CTCAGTGCAA	420
CTAAAGG	427

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTGAATTCC ACCATGCCGT GCAGCAGAGC TCTGA	35
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTGGATCCT CATAAAGGCC CTGGGTGTC	29
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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTGAATTCC ACCATGGCTC TGCAGATCCC CA

32

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGGATCCT CACTGCAGGA GCCCTGCT

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTTGCAGG ACAGGATGTG GTGCCCCGATG TGA TAGCTC TTTGCTGCAG GCCGTCCTAT	60
CCTCTGGTTC CGATAAGAGA CCGAGAACTC CGGCCCCCCA CCGCCCACCG CCACCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCAAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCCTGCAGA GACCTCCCAG AGACCAGGAT GCCGTGCAGC AGAGCTCTGA	480
TTCTGGGGGT CCTCGCCCTG AACACCATGC TCAGCCTCTG CGGAGGTGAA GACGACATTG	540
AGGCCGACCA CGTAGGCTTC TATGGTACAA CTGTTTATCA GTCTCCTGGA GACATTGGCC	600
AGTACACACA TGAATTTGAT GGTGATGAGT TGTTCTATGT GGACTTGGAT AAGAAGAAAA	660
CTGTCTGGAG GCTTCTGAG TTTGGCCAAT TGATACTCTT TGAGCCCCAA GGTGGACTGC	720
AAAACATAGC TGCAGAAAAA CACAACCTGG GAATCTTGAC TAAGAGGTCA AATTTCACCC	780
CAGCTACCAA TGAGGCTCCT CAAGCGACTG TGTTCCCCAA GTCCCCTGTG CTGCTGGGTG	840
AGCCCAACAC CCTTATCTGC TTTGTGGACA ACATCTTCCC ACCTGTGATC AACATCACAT	900
GGCTCAGGAA TAGCAAGTCA GTCACAGACG GCGTTTATGA GACCAGCTTC CTCGTCAACC	960
GTGACCATTG CTTCCACAAG CTGTCTTATC TCACCTTCAT CCCTTCTGAT GATGACATTT	1020
ATGACTGCAA GGTGGAGCAC TGGGGCCTGG AGGAGCCGGT TCTGAAACAC TGGGAACCTG	1080
AGATTCCAGC CCCCATGTCA GAGCTGACAG AAAGTGTGGT GTGTGCCCTG GGGTTGTCTG	1140
TGGGCCTTGT GGGCATCGTG GTGGGCACCA TCTTCATCAT TCAAGGCCTG CGATCAGGTG	1200
GCACCTCCAG ACACCCAGGG CCTTTATGAG TCACACCCTG GAAAGGAAGG TGTGTGTCCC	1260
TCTTCATGGA AGAAGTGGTG TTCTGGGTGT CGAATTCGAG CTCGGTACCC GGGGATCCTC	1320
TAGAGTCGAC CTGCAGGCAT GCAATTCGAT GCACACTCAC ATTCTTCTCC TAATACGATA	1380
ATAAACTTTT CCATGAAAAA TATGGAAAAA TATATGAAAA TTGAGAAATC CAAAAACTG	1440
ATAAACGCTC TACTTAATTA AAATAGATAA ATGGGAGCGG CAGGAATGGC GGAGCATGGC	1500
CAAGTTCCTC CGCCAATCAG TCGTAAAAA GAAGTCGTGG AAAGCGGATA GAAAGAATGT	1560
TCGATTGAC GGGCAAGCAT GTCTGCTATG TGGCGGATTG CGGAGGAATT GCACTGGAGA	1620
CCAGCAAGGT TCTCATGACC AAGAAATATG CGGTGAGTGA GCGGGAAGCT CGGTTTCTGT	1680
CCAGATCGAA CTCAAACTA GTCCAGCCAG TCGCTGTCTG AACTAATTAA GTAAATGAGT	1740

TTTTCATGTT AGTTTCGCGC TGAGCAACAA TTAAGTTTAT GTTTCAGTTC GGCTTAGATT	1800
TCGCTGAAGG ACTTGCCACT TTCAATCAAT ACTTTAGAAC AAAATCAAAA CTCATTCTAA	1860
TAGCTTGGTG TTCATCTTTT TTTTAAATGA TAAGCATTTT GTCGTTTATA CTTTTTATAT	1920
TTCGATATTA AACACCTAT GAAGTTCATT TTAATCGCCA GATAAGCAAT ATATTGTGTA	1980
AATATTTGTA TTCTTTATCA GGAAATTCAG GGAGACGGGG AAGTTACTAT CTACTAAAAG	2040
CCAAACAATT TCTTACAGTT TTACTCTCTC TACTCTAGAG CTTGGCACTG GCCGTCGTTT	2100
TACAACGTCG TGA CTGGGAA AACCTGGCG TTACCCAAC TAATCGCCTT GCAGCACATC	2160
CCCCTTTTCG CAGCTGGCGT AATAGCGAAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT	2220
TGCGCAGCCT GAATGGCGAA TGGCGGCTGA TGCGGTATTT TCTCCTTACG CATCTGTGCG	2280
GTATTTTACA CCGCATATGG TGA CTCTCA GTACAATCTG CTCTGATGCC GCATAGTTAA	2340
GCCAGCCCCG ACACCCGCCA ACACCCGCTG ACGCGCCCTG ACGGGCTTGT CTGCTCCCGG	2400
CATCCGCTTA CAGACAAGCT GTGACCGTCT CCGGGAGCTG CATGTGTCAG AGGTTTTTAC	2460
CGTCATCACC GAAACGCGCG AGACGAAAGG GCCTCGTGAT ACGCCTATTT TTATAGGTAA	2520
ATGTCATGAT AATAATGGTT TCTTAGACGT CAGGTGGCAC TTTTCGGGGA AATGTGCGCG	2580
GAACCCCTAT TTGTTTATTT TTCTAAATAC ATTCAAATAT GTATCCGCTC ATGAGACAAT	2640
AACCTGATA AATGCTTCAA TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTTCC	2700
GTGTGCCCCT TATTCCTTT TTTGCGGCAT TTTGCCTTCC TGTTTTTGCT CACCCAGAAA	2760
CGCTGGTGAA AGTAAAAGAT GCTGAAGATC AGTTGGGTGC ACGAGTGGGT TACATCGAAC	2820
TGGATCTCAA CAGCGTAAG ATCCTTGAGA GTTTTCGCCC CGAAGAACGT TTTCCAATGA	2880
TGAGCACTTT TAAAGTTCTG CTATGTGGCG CGGTATTATC CCGTATTGAC GCCGGGCAAG	2940
AGCAACTCGG TCGCCGCATA CACTATTCTC AGAATGACTT GGTGAGTAC TCACCAGTCA	3000
CAGAAAAGCA TCTTACGGAT GGCATGACAG TAAGAGAATT ATGCAGTGCT GCCATAACCA	3060
TGAGTGATAA CACTGCGGCC AACTTACTTC TGACAACGAT CGGAGGACCG AAGGAGCTAA	3120
CCGCTTTTTT GCACAACATG GGGGATCATG TAACTCGCCT TGATCGTTGG GAACCGGAGC	3180
TGAATGAAGC CATACCAAAC GACGAGCGTG ACACCACGAT GCCTGTAGCA ATGGCAACAA	3240
CGTTGCGCAA ACTATTAAC TGGCAACTAC TTACTCTAGC TTCCCGGCAA CAATTAATAG	3300
ACTGGATGGA GGGCGATAAA GTTGCAAGAC CACTTCTGCG CTCGGCCCTT CCGGCTGGCT	3360
GGTTTATTGC TGATAAATCT GGAGCCGGTG AGCGTGGGTC TCGCGGTATC ATTGCAGCAC	3420
TGGGGCCAGA TGGTAAGCCC TCCCGTATCG TAGTTATCTA CACGACGGGG AGTCAGGCAA	3480
CTATGGATGA ACGAAATAGA CAGATCGCTG AGATAGGTGC CTCACTGATT AAGCATTTGGT	3540
AACTGTCAGA CCAAGTTTAC TCATATATAC TTTAGATTGA TTTAAACTT CATTTTTAAT	3600
TTAAAAGGAT CTAGGTGAAG ATCCTTTTTG ATAATCTCAT GACCAAAATC CCTTAACGTG	3660
AGTTTTTCGT CCACTGAGCG TCAGACCCCG TAGAAAAGAT CAAAGGATCT TCTTGAGATC	3720
CTTTTTTCT GCGCGTAATC TGCTGCTTGC AAACAAAAA ACCACCGCTA CCAGCGGTGG	3780
TTTGTTCGCC GGATCAAGAG CTACCAACTC TTTTCCGAA GGTAAGTGGC TTCAGCAGAG	3840
CGCAGATACC AAATACTGTC CTTCTAGTGT AGCCGTAGTT AGGCCACCAC TTCAAGAACT	3900
CTGTAGCACC GCCTACATAC CTCGCTCTGC TAATCCTGTT ACCAGTGGCT GCTGCCAGTG	3960
GCGATAACTC GTGTCTTACC GGGTTGGACT CAAGACGATA GTTACCGGAT AAGGCGCAGC	4020
GGTCGGGCTG AACGGGGGT TCGTGCACAC AGCCAGCTT GGAGCGAAGC ACCTACACCG	4080

AACTGAGATA CCTACAGCGT GAGCATTGAG AAAGCGCCAC GCTTCCCGAA GGGAGAAAGG	4140
CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA GCGCACGAGG GAGCTTCCAG	4200
GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC	4260
GATTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGGAA AAACGCCAGC AACGCGGCCT	4320
TTTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCACAT GTTCTTTCCT GCGTTATCCC	4380
CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT CGCCGCAGCC	4440
GAACGACCGA GCGCAGCGAG TCAGTGAGCG AGGAAGCGGA AGAGCGCCCA ATACGCAAAC	4500
CGCCTCTCCG CGCGCGTTGG CCGATTCAAT AATGCAGCTG GCACGACAGG TTTCCCGACT	4560
GGAAAGCGGG CAGTGAGCGC AACGCAATTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC	4620
AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC GGATAACAAT	4680
TTCACACAGG AAACAGCTAT GACCATGATT ACG	4713

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGTTGCAGG ACAGGATGTG GTGCCCCGATG TGACTAGCTC TTTGCTGCAG GCGGTCTTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCA CCGCCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCTTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCCCTGCTG TGCCCTAGAG ATGGCTCTGC AGATCCCAG CCTCCTCCTC	480
TCAGCTGCTG TGGTGGTGCT GATGGTGCTG AGCAGCCCAG GGAAGTGGG CGGAAACTCC	540
GAAAGGCATT TCGTGGTCCA GTTCAAGGGC GAGTGCTACT ACACCAACGG GACGCAGCGC	600
ATACGGCTCG TGACCAGATA CATCTACAAC CGGGAGGAGT ACGTGCGCTA CGACAGCGAC	660
GTGGGCGAGT ACCGCGCGGT GACCGAGCTG GGGCGGCCAG ACGCCGAGTA CTGGAACAGC	720

CAGCCGGAGA TCCTGGAGCG AACGCGGGCC GAGGTGGACA CGGCGTGCAG ACACAACACTAC	780
GAGGGGCGCG AGACCAGCAC CTCCCTGCGG CGGCTTGAAC AGCCCAATAT CGCCATCTCC	840
CTGTCCAGGA CAGAGGCCCT CAACCACCAC AACACTCTGG TCTGTTCCGT GACAGATTTC	900
TACCCAGCCA AGATCAAAGT GCGCTGGTTC AGGAATGGCC AGGAGGAGAC AGTGGGGGTC	960
TCATCCACAC AGCTTATTAG GAATGGGGAC TGGACCTTCC AGGTCTGTGT CATGCTGGAG	1020
ATGACCCCTC ATCAGGGAGA GGTCTACACC TGCCATGTGG AGCATCCCAG CCTGAAGAGC	1080
CCCATCACTG TGGAGTGGAG GGCACAGTCC GAGTCTGCCC GGAGCAAGAT GTTGAGCGGC	1140
ATCGGGGGCT GCGTGTCTGG GGTGATCTTC CTCGGGCTCG GCCTTTTTCAT CCGTCACAGG	1200
AGTCAGAAAG GACCTCGAGG CCCTCCTCCA GCAGGGCTCC TGCAGTGAAT CAGACTGTTT	1260
TGACTCAGTT GACTGTCTCA GACTGTAAGA CCTACATGTC TCGAATTCGA GCTCGGTACC	1320
CGGGGATCCT CTAGAGTCGA CCTGCAGGCA TGCAATTGGA TGCACACTCA CATTCTTCTC	1380
CTAATACGAT AATAAACTT TCCATGAAAA ATATGGAAAA ATATATGAAA ATTGAGAAAT	1440
CCAAAAAAT GATAAACGCT CTACTTAATT AAAATAGATA AATGGGAGCG GGAGGAATGG	1500
CGGAGCATGG CCAAGTTCCT CCGCCAATCA GTCGTAAAAAC AGAAGTCGTG GAAAGCGGAT	1560
AGAAAGAATG TTCGATTGTA CGGGCAAGCA TGTCTGTCTAT GTGGCGGATT GCGGAGGAAT	1620
TGCACTGGAG ACCAGCAAGG TTCTCATGAC CAAGAATATA GCGGTGAGTG AGCGGGAAGC	1680
TCGGTTTCTG TCCAGATCGA ACTCAAACT AGTCCAGCCA GTCGCTGTG AACTAATTA	1740
AGTAAATGAG TTTTTCATGT TAGTTTCGCG CTGAGCAACA ATTAAGTTTA TGTTTCAGTT	1800
CGGCTTAGAT TTCGCTGAAG GACTTGCCAC TTTCAATCAA TACTTTAGAA CAAAATCAAA	1860
ACTCATTCTA ATAGCTTGGT GTTCATCTTT TTTTAAATG ATAAGCATT TGTCTTTAT	1920
ACTTTTTATA TTTGATATT AAACCACCTA TGAAGTTCAT TTTAATCGCC AGATAAGCAA	1980
TATATTGTGT AAATATTGT ATTCTTTATC AGGAAATTC GGGAGACGGG GAAGTTACTA	2040
TCTACTAAAA GCCAAACAAT TTCTTACAGT TTTACTCTCT CTACTCTAGA GCTTGGCACT	2100
GGCGTCTGTT TTACAACGTC GTGACTGGGA AAACCTGGC GTTACCCAAC TTAATCGCCT	2160
TGCAGCACAT CCCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATCGCCC	2220
TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGCGCCTG ATGCGGTATT TTCTCCTTAC	2280
GCATCTGTGC GGTATTTTAC ACCGCATATG GTGCACTCTC AGTACAATCT GCTCTGATGC	2340
CGCATAGTTA AGCCAGCCCC GACACCCGCC AACACCCGCT GACGCGCCCT GACGGGCTTG	2400
TCTGCTCCCG GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT GCATGTGTCA	2460
GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGACGAAAG GGCCTCGTGA TACGCCTATT	2520
TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG TCAGGTGGCA CTTTTCGGGG	2580
AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCCGCT	2640
CATGAGACAA TAACCCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT	2700
TCAACATTTC CGTGTGCGCC TTATTCCCTT TTTTGGCGCA TTTTGCCTTC CTGTTTTTGC	2760
TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG CACGAGTGGG	2820
TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACG	2880
TTTTCCAATG ATGAGCACTT TTAAAGTTCT GCTATGTGGC GCGGTATTAT CCCGTATTGA	2940
CGCCGGGCAA GAGCAACTCG GTCGCGCAT AACTATTCT CAGAATGACT TGGTTGAGTA	3000
CTCACCAGTC ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC	3060

TGCCATAACC	ATGAGTGATA	ACACTGCGGC	CAACTTACTT	CTGACAACGA	TCGGAGGACC	3120
GAAGGAGCTA	ACCGCTTTTT	TGCACAACAT	GGGGGATCAT	GTAAC TCGCC	TTGATCGTTG	3180
GGAACCGGAG	CTGAATGAAG	CCATACCAAA	CGACGAGCGT	GACACCACGA	TGCCTGTAGC	3240
AATGGCAACA	ACGTTGCGCA	AACTATTAAC	TGGCGAACTA	CTTACTCTAG	CTTCCCGGCA	3300
ACAATTAATA	GA CTGGATGG	AGGCGGATAA	AGTTGCAGGA	CCACTTCTGC	GCTCGGCCCT	3360
TCCGGCTGGC	TGGTTTATTG	CTGATAAATC	TGGAGCCGGT	GAGCGTGGGT	CTCGCGGTAT	3420
CATTGCAGCA	CTGGGGCCAG	ATG GTAAGCC	CTCCCGTATC	G TAGTTATCT	ACACGACGGG	3480
GAGTCAGGCA	ACTATGGATG	AACGAAATAG	ACAGATCGCT	GAGATAGGTG	CCTCACTGAT	3540
TAAGCATTGG	TA ACTGTCAG	ACCAAGTTTA	CTCATATATA	CTTTAGATTG	ATTTAAAACT	3600
TCATTTTAA	TTTAAAAGGA	TCTAGGTGAA	GATCCTTTTT	GATAATCTCA	TGACCAAAAT	3660
CCCTTAACGT	GAGTTTTCGT	TCCACTGAGC	GTCAGACCCC	G TAGAAAAGA	TCAAAGGATC	3720
TTCTTGAGAT	CCTTTTTTTC	TGCGCGTAAT	CTGCTGCTTG	CAAACAAAAA	AACCACCGCT	3780
ACCAGCGGTG	GTTTGTTTGC	CGGATCAAGA	GCTACCAACT	CTTTTCCGA	AGGTA ACTGG	3840
CTTCAGCAGA	GCGCAGATAC	CAAATACTGT	CCTTCTAGTG	TAGCCGTAGT	TAGGCCACCA	3900
CTTCAAGAAC	TCTGTAGCAC	CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCACTGGC	3960
TGCTGCCAGT	GGCGATAAGT	CGTGTCTTAC	CGGGTTGGAC	TCAAGACGAT	AGTTACCGGA	4020
TAAGGCGCAG	CGGTCGGGCT	GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC	4080
GACCTACACC	GA ACTGAGAT	ACCTACAGCG	TGAGCATTGA	GAAAGCGCCA	CGCTTCCCGA	4140
AGGGAGAAAG	GCGGACAGGT	ATCCGGTAAG	CGGCAGGGTC	GGAACAGGAG	AGCGCACGAG	4200
GGAGCTTCCA	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	GTCGGGTTTC	GCCACCTCTG	4260
ACTTGAGCGT	CGATTTTGT	GATGCTCGTC	AGGGGGGCGG	AGCCTATGGA	AAAACGCCAG	4320
CAACGCGGCC	TTTTTACGGT	TCCTGGCCTT	TTGCTGGCCT	TTTGCTCACA	TGTTCTTTCC	4380
TGCGTTATCC	CCTGATTCTG	TGGATAACCG	TATTACGGCC	TTTGAGTGAG	CTGATACCGC	4440
TGCGCGCAGC	CGAACGACCG	AGCGCAGCGA	GTCAGTGAGC	GAGGAAGCGG	AAGAGCGCCC	4500
AATACGCAAA	CGCCTCTCC	CGGCGCGTTG	GCCGATTCAT	TAATGCAGCT	GGCAGCACAG	4560
GTTTCCCGAC	TGGAAAGCGG	GCAGTGAGCG	CAACGCAATT	AATGTGAGTT	AGCTCACTCA	4620
TTAGGCACCC	CAGGCTTTAC	ACTTTATGCT	TCCGGCTCGT	ATGTTGTGTG	GAATTGTGAG	4680
CGGATAACAA	TTTACACAG	GAAACAGCTA	TGACCATGAT	TACG		4724

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACCATGGC CATTAGTGGA GTC

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGGATCCT TACAGAGGCC CCCTGCGTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACCATGGT GTGTCTGAGG CTCC

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGGATCCT CAGCTCAGGA ATCCTCTTG

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCACCATGGT CCTAAACAAA GCTCTGAT

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTGGATCCT CACAAGGGCC CTGGTGTCT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCACCATGGC TTGAAGAAG GCCTTT

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTAGATCTC AGTGCAGAAG CCCTTT

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACCATGGG CCCTGAAGAC AGAAT

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTGATCCT CACAGGGTCC CCTGGGC

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACCATGGT TCTGCAGGT TCTGCG

26

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTGGATCCT TATGCAGATC CTCGTTGAA

29

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGAATTCAC TAGAGGCTAG AGCCAT

26

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGGATCCTC ACAGGGTGAC TTGACC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2580 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGGTTGCAGG	ACAGGATGTG	GTGCCCAGATG	TGACTAGCTC	TTTGCTGCAG	GCCGTCCTAT	60
CCTCTGGTTC	CGATAAGAGA	CCCAGAACTC	CGGCCCCCCA	CCGCCCACCG	CCACCCCAT	120
ACATATGTGG	TACGCAAGTA	AGAGTGCTTG	CGCATGCCCC	ATGTGCCCCA	CCAAGAGTTT	180
TGCATCCCAT	ACAAGTCCCC	AAAGTGGAGA	ACCGAACCAA	TTCTTCGCGG	GCAGAACAAA	240
AGCTTCTGCA	CACGTCTCCA	CTCGAATTTG	GAGCCGGCCG	GCGTGTGCAA	AAGAGGTGAA	300
TGAACGAAA	GACCCGTGTG	TAAAGCCGCG	TTTCCAAAAT	GTATAAAACC	GAGAGCATCT	360
GGCCAATGTG	CATCAGTTGT	GGTCAGCAGC	AAAATCAAGT	GAATCATCTC	ACTGCAACTA	420
AAGGGGGGAA	TTGATCTAG	AGGCTAGAGC	CATGGATGAC	CAACGCGACC	TCATCTCTAA	480
CCATGAGCAA	TTGCCCATAC	TGGGCAACCG	CCCTAGAGAG	CCAGAAAGGT	GCAGCCGTGG	540
AGCTCTGTAC	ACCGGTGTTT	CTGTCTGTTT	GGCTCTGCTC	TTGGCTGGGC	AGGCCACAC	600
TGCTTACTTC	CTGTACCAGC	AACAGGGCCG	CCTAGACAAG	CTGACCATCA	CCTCCAGAA	660
CCTGCAACTG	GAGAGCCTTC	GCATGAAGCT	TCCGAAATCT	GCCAAACCTG	TGAGCCAGAT	720
GCGGATGGCT	ACTCCCTTGC	TGATGCGTCC	AATGTCCATG	GATAACATGC	TCCTTGGGCC	780
TGTGAAGAAC	GTTACCAAGT	ACGGCAACAT	GACCCAGGAC	CATGTGATGC	ATCTGCTCAC	840
GAGGTCTGGA	CCCCTGGAGT	ACCCGCAGCT	GAAGGGGACC	TTCCAGAGA	ATCTGAAGCA	900
TCTTAAGAAC	TCCATGGATG	GCGTGAAGT	GAAGATCTTC	GAGAGCTGGA	TGAAGCAGTG	960
GCTCTTGTTT	GAGATGAGCA	AGAACTCCCT	GGAGGAGAAG	AAGCCCACAG	AGGCTCCACC	1020
TAAAGAGCCA	CTGGACATGG	AAGACCTATC	TTCTGGCCTG	GGAGTGACCA	GGCAGGAACT	1080
GGGTCAAGTC	ACCCTGTGAA	GACAGAGGCC	AGCATCAAGC	TTATCGATAC	CCTCGACCTG	1140
CAGGCATGCA	ATTGATGCA	CACTCACATT	CTTCTCCTAA	TACGATAATA	AAACTTTCCA	1200
TGAAAAATAT	GGAAAAATAT	ATGAAAAATTG	AGAAATCCAA	AAAAGTATA	AACGCTCTAC	1260
TTAATTAATA	TAGATAAATG	GGAGCGGCAG	GAATGGCGGA	GCATGGCCAA	GTTCTCTCCG	1320
CAATCAGTCG	TAAACAGAA	GTCGTGAAA	GCGGATAGAA	AGAATGTTTG	ATTTGACGGG	1380
CAAGCATGTC	TGCTATGTGG	CGGATTGCGG	AGGAATTGCA	CTGGAGACCA	GCAAGGTTCT	1440
CATGACCAAG	AATATAGCGG	TGAGTGAGCG	GGAAGCTCGG	TTTCTGTCCA	GATCGAACTC	1500
AAAAGTAGTC	CAGCCAGTCG	CTGTGAAAC	TAATTAAGTA	AATGAGTTTT	TCATGTTAGT	1560
TTGCGGCTGA	GCAACAATTA	AGTTTATGTT	TCAGTTGCGC	TTAGATTTTG	CTGAAGGACT	1620
TGCCACTTTC	AATCAATACT	TTAGAACAAA	ATCAAACTC	ATTCTAATAG	CTTGGTGTTC	1680
ATCTTTTTTT	TTAATGATAA	GCATTTTGTC	GTTTATACTT	TTTATATTTT	GATATTAAAC	1740
CACCTATGAA	GTTTATTTTA	ATCGCCAGAT	AAGCAATATA	TTGTGTAAAT	ATTTGTATTC	1800
TTTATCAGGA	AATTCAGGGA	GACGGGGAAG	TTACTATCTA	CTAAAAGCCA	AACAATTTCT	1860
TACAGTTTTA	CTCTCTCTAC	TCTAGAGCTT	GGCACTGGCC	GTCGTTTTAC	AACGTCGTGA	1920
CTGGGAAAAC	CCTGGCGTTA	CCCAACTTAA	TGCGCTTGCA	GCACATCCCC	CTTTCGCCAG	1980
CTGGCGTAAT	AGCGAAGAGG	CCCGCACCGA	TGCGCTTCC	CAACAGTTGC	GCAGCCTGAA	2040
TGGCGAATGG	CGCCTGATGC	GGTATTTTCT	CCTTACGCAT	CTGTGCGGTA	TTTCACACCG	2100

CATATGGTGC ACTCTCAGTA CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGCCCCGACA	2160
CCCCCAACA CCCGCTGACG CGCCCTGACG GGCTTGTCTG CTCCCGGCAT CCGCTTACAG	2220
ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT GTGTCAGAGG TTTTCACCGT CATCACCGAA	2280
ACGCGCGAGA CGAAAGGGCC TCGTGATACG CCTATTTTTA TAGGTTAATG TCATGATAAT	2340
AATGGTTTCT TAGACGTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA CCCCTATTTG	2400
TTTATTTTTC TAAATACATT CAAATATGTA TCCGCTCATG AGACAATAAC CCTGATAAAT	2460
GCTTCAATAA TATTGAAAAA GGAAGAGTAT GAGTATTCAA CATTTCCGTG TCGCCCTTAT	2520
TCCCTTTTTT GCGGCATTTT GCCTTCCTGT TTTTGCTCAC CCAGAAACGC TGGTGAAAGT	2580

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAGAATTCAC CATGGATGAT CAGCGCGACC TT

32

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAAGGATCCT CACATGGGGA CTGGGCCAG A

31

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACCATGGG TCATGAACAG AACCA

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTTGTCGACT CAGTCACCTG AGCAAGG

27

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAACGATGGT CTCATTCCTG CC

22

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTGTCGACC TAGGAAATGT GCCATCC

27

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTAGAATTC ACCATGGCTT CAACCGGTGC CAAG

34

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTAGTCGAC TCAGGGAGGT GGGGCTTGTC C

31

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACCCTTGAAT TCATGGCTCC CAGCAGCCCC CGGCCC

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATTACCGGAT CCTCAGGGAG GCGTGGCTTG TGTGTTGG

39

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGGTACCCG TGGAGACTGC CAGAGAT

27

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTTGATCCC TATGGCCGGA AGGCCTG

27

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGAATTCCT GTCAGAATGG CCACCAT

27

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTAGATCTT CACTCAGCTC TGGACGGT

28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCCTTGAGC TCATGGTTGC TGGGAGCGAC GCGGGG

36

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATTACCGGAT CCTTAAAGAA CATTATATA CAGCACAATA CA

42

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTAGAATTC ACCATGGCTT GCAATTGTCA GTTG

34

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTAGTCGAC CTAAAGGAAG ACGGTCTGTT C

31

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCCTTGAAT CCATGGGCCA CACACGGAGG CAG

33

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATTACCGGAT CCTTATACAG GCGGTACACT TTCCCTTCT

39

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTAGAATTC ACCATGGACC CCAGATGCAC CATGGG

36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTTAGTCGAC TCACTCTGCA TTTGGTTTTG CTGA

34

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACCCTTGAGC TCATGGATCC CCAGTGCACT ATG

33

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTACCCCCG GGTAAAAAC ATGTATCACT TTTGTGGCAT GA

42

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAGGATCCA CCATGCAGCA GCCCTTCAAT T

31

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTGGATCCT TAGAGCTTAT ATAAGCCGA

29

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAAGAATTTCG GTACCATGCC GGAGGAGGCT TCGG

34

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTGGATCCT CAGGGGCGCA CCCACTGCA

29

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile	Ser	Gln	Ala	Val	His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly
1				5					10					15	

Arg

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Lys Thr Ile Ala Thr Asp Glu Glu Ala Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe	Val	Arg	Phe	Asp	Ser	Asp	Ala	Ala	Ser	Gln	Arg	Met
1				5					10			